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279152RX
SEQUENCE LISTING

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<140> 09/825,882

<141> 2001-04-05

<150> 60/195,532

<151> 2000-04-07

<150> 60/247,014

<151> 2000-11-13

<160> 31

<170> PatentIn Ver. 2.1

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Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
50 55 60

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Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
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Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
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Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
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Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
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Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
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Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
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180 185 190

Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
195 200 205

Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
210 215 220

Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
225 230 235 240

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245 250 255

Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
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Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
275 280 285

Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
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Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
50 55 60

Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
65 70 75 80

Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
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Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
100 105 110

Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
115 120 125

Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
130 135 140

Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
145 150 155 160

Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
165 170 175

Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
180 185 190

Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
195 200 205

Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
210 215 220

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Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
225 230 235 240

Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
245 250 255

Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
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Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
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Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
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35 40 45

Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
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55

60

Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
65 70 75 80

Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
85 90 95

Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
100 105 110

Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
115 120 125

Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
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Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
165 170 175

Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
180 185 190

Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
195 200 205

Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
210 215 220

Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
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245 250 255

Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
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Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
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Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
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Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Asn Ser Val Glu Val
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Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
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Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
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Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
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Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
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Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
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165 170 175

Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
180 185 190

Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile 279152RX
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 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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 35 40 45
 Ala Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
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Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
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Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
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Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
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Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
115 120 125

Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
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Phe Val Ile Asn Met Lys Glu Ile Val Arg Thr Lys Glu Tyr Glu Gly
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Asn Leu Thr Trp Lys Ile Lys Leu Arg Ser Ala Val Tyr Leu Ser Asp
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Ala Thr Val Thr Thr Leu Gly Asn Leu Val Pro Phe Thr Leu Thr Leu
180 185 190

Leu Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Phe Phe Leu Leu Leu Cys Ala Val
225 230 240

Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
245 250 255

Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
Page 9

260 279152RX 270

Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
275 280 285

Thr Phe Leu Ser Val Leu Arg Gln Val Arg Tyr Trp Val Lys Gly Glu
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Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe
50 55 60

Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val
65 70 75 80

Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met
85 90 95

Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val
Page 10

115 120 279152RX 125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
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 Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175
 Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
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 Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
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 Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
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 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240
 Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln
 245 250 255
 Ser Lys Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro
 260 265 270
 Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Leu Trp Gln Met Thr Arg
 290 295

<210> 15
<211> 900
<212> DNA
<213> *Homo sapiens*

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<400> 15
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atcccttcag ctgaccaaatt tctcaactgt ctggcggctc ccagaattgg tttgctctgg 180
gcattattat taaattggta ttaactgtg ttgaaatccag ctttttatag tttttagat 240
agaattactt ctatataatgc ctgggttgta accaaccatt tcagcatgt gcttgcgtct 300
aacctcgaca tatttttattt gctcaagatt gccaaccattt ccaaccttct ttttcttcat 360
ttaaagagggag gaggtagggat tgcatttctg gtgatactgt tggggacttt gatattttt 420
gtttgtcattt ttcttgtggc aaacatggat gagagtatgt gggcagaaga atatgaagga 480
aacatgactg ggaagatgaa attgaggaat acagtagatc tttcatattt gactgtact 540
accctatggaa gcttcatacc ctttacttctg tccctgatatt cttttctgtat gctaattctgt 600
tctctgtgtt aacatctcaa gaagatgcag ctccatggag aaggatgcga agatctcagc 660
accaagggtcc acataaaagc ttgcacaattt ctgtatctctt tcccttctgtt atgtccatt 720
ttctttctat tcctaatcgt ttgggttgg agtcccttagga ggctcgcgaa tgaccgggtt 780
gtcatggtta gcaaggctgt tggaaacata tatcttgcatt tcgactcatt catccattt 840
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<210> 16
<211> 299
<212> PRT
<213> *Homo sapiens*

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<400> 16
Met Ile Thr Phe Leu Tyr Ile Phe Phe Ser Ile Leu Ile Met Val Leu
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Phe Val Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Phe
20 25 30
Ile Asp Trp Val Lys Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu
35 40 45
Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu
50 55 60
Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
65 70 75 80
Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met
85 90 95
Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110
Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val
115 120 125
Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu
130 135 140
Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly
145 150 155 160
Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr
165 170 175
Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu
180 185 190
Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205
Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
210 215 220
Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Cys Ala Ile
225 230 235 240
Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
245 250 255
Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
260 265 270
Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
275 280 285
Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
290 295

<210> 17
<211> 924
<212> DNA

<213> Homo sapiens

<400> 17

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ttgctccct	tggatatgt	cctcattagc	ttgggtgcct	cccgcttctg	cctgcagttg	180
gttggacgg	tgcacaacct	ctactactct	gcccagaagg	tcgagtaactc	tgggggtctc	240
ggccgacagt	tcttccatct	acactggcac	ttcctgaact	cagccacactt	ctgggtttgc	300
agctggctca	gtgtccgtt	ctgtgtgaag	attgctaaca	tcacacactc	caccctcctg	360
tggctgaagt	ggagggtccc	agggtgggtg	ccctggctcc	tgtggggctc	tgtcctgatc	420
tccttcata	taaccctgt	gttttttg	gtgaactacc	ctgtatata	agaattttta	480
attagaaaat	tttctggaa	catgacccat	aagtggataa	caaggataga	aacatactat	540
ttcccatcccc	tgaaactgg	catctggtca	attcctttt	ctgtttttct	ggtctcaatt	600
atgctgtta	ttaattctct	gaggaggcat	actcagagaa	tgcagcaca	cgggcacagc	660
ctgcaggacc	ccagcaccca	ggctcacacc	agactctga	agtccctcat	ctccctcctc	720
attcttatg	tctgtccctt	tctgtccctg	atcattgtat	ccgcaaaatt	tatccatcg	780
cagaacgact	tttactggcc	atggcaaatt	gcagtctacc	tgtgcatatc	tgtccatccc	840
ttcatcctca	tcttcagca	cctcaagctt	cgaagcgtgt	tctcgcagct	cctgttgtt	900
gcaaggggct	tctgggtggc	ctag				924

<210> 18

<211> 307

<212> PRT

<213> Homo sapiens

<400> 18

Met	Gln	Ala	Ala	Leu	Thr	Ala	Phe	Phe	Val	Leu	Leu	Phe	Ser	Leu	Leu
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Ser	Leu	Leu	Gly	Ile	Ala	Ala	Asn	Gly	Phe	Ile	Val	Leu	Val	Leu	Gly
				20				25					30		

Arg	Glu	Trp	Leu	Arg	Tyr	Gly	Arg	Leu	Leu	Pro	Leu	Asp	Met	Ile	Leu
							35	40					45		

Ile	Ser	Leu	Gly	Ala	Ser	Arg	Phe	Cys	Leu	Gln	Leu	Val	Gly	Thr	Val
						50		55				60			

His	Asn	Phe	Tyr	Tyr	Ser	Ala	Gln	Lys	Val	Glu	Tyr	Ser	Gly	Gly	Leu
							65	70		75			80		

Gly	Arg	Gln	Phe	Phe	His	Leu	His	Trp	His	Phe	Leu	Asn	Ser	Ala	Thr
						85		90				95			

Phe	Trp	Phe	Cys	Ser	Trp	Leu	Ser	Val	Leu	Phe	Cys	Val	Lys	Ile	Ala
						100		105				110			

Asn	Ile	Thr	His	Ser	Thr	Phe	Leu	Trp	Leu	Lys	Trp	Arg	Phe	Pro	Gly
						115		120				125			

Trp	Val	Pro	Trp	Leu	Leu	Leu	Gly	Ser	Val	Leu	Ile	Ser	Phe	Ile	Ile
						130		135			140				

Thr	Leu	Leu	Phe	Phe	Trp	Val	Asn	Tyr	Pro	Val	Tyr	Gln	Glu	Phe	Leu
						145		150			155			160	

Ile	Arg	Lys	Phe	Ser	Gly	Asn	Met	Thr	Tyr	Lys	Trp	Asn	Thr	Arg	Ile
						165		170			175				

Glu	Thr	Tyr	Tyr	Phe	Pro	Ser	Leu	Lys	Leu	Val	Ile	Trp	Ser	Ile	Pro
						180		185			190				

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Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
195 200 205

Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
210 215 220

Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
225 230 235 240

Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
245 250 255

Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
260 265 270

Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
275 280 285

Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe
290 295 300

Trp Val Ala
305

<210> 19

<211> 930

<212> DNA

<213> Homo sapiens

<400> 19

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atctcttttgc ctgaccataat tctcaactgct ctggcagtct ccagagttgg tttactctgg 180
gtatttagtat taaattggta tgcaactgag ttgaatccag ctttaacag tatagaagta 240
agaattactg cttacaatgt ctgggcagta atcaaccatt tcagcaactg gcttgcact 300
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gtttgtcatc tttttgtat aaacatgaat cagattatgg acatggatggat gatggaaaggaa 480
aacatgactt ggaagatcaa actgaggagt gcaatgttacc tttcaataac aacggtaacc 540
atccttagcaa acttagttcc cttcaactctg accctgatat cttttctgtt gttatctgt 600
tctctgtgtca aacatctcaa aaagatgcag ctccatggca aaggatctca agatcccagc 660
atgaagggtcc acataaaaggc tttgcaact gtgacccctt tcctcttgc atgtgccatt 720
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<210> 20

<211> 309

<212> PRT

<213> Homo sapiens

<400> 20

Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
1 5 10 15

Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20 25 30

Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
35 40 45

279152RX

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Val Leu
50 55 60

Asn Trp Tyr Ala Thr Glu Leu Asn Pro Ala Phe Asn Ser Ile Glu Val
65 70 75 80

Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Ile Asn His Phe Ser Asn
85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
130 135 140

Phe Val Ile Asn Met Asn Gln Ile Ile Trp Thr Lys Glu Tyr Glu Gly
145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr Leu Ser Asn
165 170 175

Thr Thr Val Thr Ile Leu Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
180 185 190

Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Met Lys Val His
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
225 230 235 240

Tyr Phe Leu Ser Ile Ile Met Ser Val Trp Ser Phe Glu Ser Leu Glu
245 250 255

Asn Lys Pro Val Phe Met Phe Cys Glu Ala Ile Ala Phe Ser Tyr Pro
260 265 270

Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
275 280 285

Thr Phe Leu Ser Val Leu Trp His Val Arg Tyr Trp Val Lys Gly Glu
290 295 300

Lys Pro Ser Ser Ser
305

<210> 21
<211> 930
<212> DNA
<213> Homo sapiens

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atctcctcag ctgaccataat cctcactgct ctgggttgtct ccagaatggg tttactctgg 180
gtcatattat tacattggta tgcaaattgtg tttaattcag ctttatatacg ttcagaagta 240

279152RX

ggagctgttg	cttctaata	ctcagaata	atcaaccatt	ttagcatctg	gcttgctgct	300
agcctcagca	tattttat	gctcaagatt	gccaatttct	ccaaaccttat	tttctccac	360
ctaaaagaaga	gaatttaggag	tgttgttctg	gtgatactgt	tgggtccctt	gttatttttg	420
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aatgtgactt	ggaaagatcaa	attggaaat	gcaatacac	tttcaaacctt	gactgtaa	540
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accaagggtcc	acataaaagc	tttgcactt	gtgatctcct	tcctcatgtt	atatgccatt	720
tactttctgt	atctaatcac	attaacctgg	aatcttggaa	cacagcagaa	caaacttga	780
ttccctgttt	gccaaactct	tggaaatctg	tatcccttcat	tccactcatt	cttccctgatt	840
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<210> 22

<211> 885

<212> DNA

<213> Homo sapiens

<400> 22

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atctcatcg	ctgaccaa	ttctca	tctgtggtg	tccagat	gttactctg	180
ggtcatatta	ttacatttgt	atgcaact	gtttaatttg	gcttcacata	gattagaagt	240
aagaattttt	ggttcta	tctcagca	aaccaggat	ttcagcat	gggtgttact	300
agcctcagca	tatttcattt	gctcaagact	gccaatttct	ccaacccat	tttctccac	360
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atttgtatc	ttgtctgtat	aaccacgggt	gagagtgtgt	ggacaaaaga	atatgaagga	480
aatttgtctt	ggatgatcaa	attggat	gcaatacagc	tttcaaact	gactgtacc	540
atgccagcaa	acgtcacacc	ctgcact	acactaatat	ctttctgt	gttaatctat	600
tctccatgt	aacatgtcaa	gaagatgcag	ctccatggca	aggatctca	acatctcagc	660
accaaagggtc	acataaaaggc	tttgc	gtgatctct	tcctttagt	atttgcatt	720
tactttctgt	gtctaatcac	atcaact	aatccttagga	ctcagcagag	caaacttgta	780
ttccgtcttt	accaaaactct	tggattcat	tatctttgt	tccactcatt	catccgtact	840
atgggaagta	ggaagccaaa	acagac	tttcagctt	tgtga		885

<210> 23

<211> 912

<212> DNA
<213> Mu-2

<213> Mus sp.

<400> 23

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acgttcttga	tccctgcagac	ccttcttgatg	tgcacagggc	tgtccaggat	cggctgcag	180
ataatgccta	tgaccggaaag	cttcttcctt	gttttcttgc	cataactctta	tgaggaaaaat	240
atttatagtt	cagatataat	gttcgtctgg	atgttcttca	gctcgattgg	cctctgggtt	300
gccacatgtc	tctctgtctt	ttactgcctc	aagatttcag	gtttcaactcc	acctgggtt	360
cttggctgt	aattcagaat	ttcaaagctc	atattttggc	tgtcttcgtgg	cagcttgcgt	420
gcctctctgg	gcactgcaac	tgtgtgcatc	gaggtaggtt	tccctttaat	tgaggatggc	480
tatgtccctga	gaaacgcagg	actaaatgat	agaatagcca	agctagtgaa	aaataatgac	540
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ttctttttttt	cttactttgc	tgccttcatg	gcaaatatga	catttagat	tccatcagaa	780
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<210> 24

<211> 303

279152RX

<212> PRT
<213> Mus sp.

<400> 24
Met Thr Ser Pro Phe Pro Ala Ile Tyr His Met Val Ile Met Thr Ala
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Cys Tyr Asp Leu Phe Lys Ser Arg Thr Phe Leu Ile Leu Gln Thr Leu
35 40 45
Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met
50 55 60
Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn
65 70 75 80
Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile
85 90 95
Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
100 105 110
Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser
115 120 125
Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly
130 135 140
Thr Ala Thr Val Cys Ile Glu Val Gly Phe Pro Leu Ile Glu Asp Gly
145 150 155 160
Tyr Val Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val
165 170 175
Arg Asn Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Pro Leu
180 185 190
Ser Val Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys
195 200 205
His Met His Trp Met Gln Ser Glu Ser His Lys Leu Ser Ser Ala Arg
210 215 220
Thr Glu Ala His Ile Asn Ala Leu Lys Thr Val Thr Thr Phe Phe Cys
225 230 235 240
Phe Phe Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg
245 250 255
Ile Pro Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala
260 265 270
Ala Tyr Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys
275 280 285
Phe Lys Asp Leu Phe Arg Arg Met Ile Cys Leu Gln Lys Glu Glu
290 295 300

<210> 25

279152RX

<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (2)
<223> Phe or Gly

<220>
<221> MOD_RES
<222> (3)
<223> Ile, Val or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (6)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Leu or Val

<220>
<221> MOD_RES
<222> (10)
<223> Gly or Thr

<220>
<221> MOD_RES
<222> (13)
<223> Val or Ala

<220>
<221> MOD_RES
<222> (18)
<223> Ile or Met

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 25
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1 5 10 15

Cys Xaa Asp Trp
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<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES

279152RX

<222> (1)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (2)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (3)
<223> Ile or Leu

<220>
<221> MOD_RES
<222> (5)
<223> Thr or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Gly, Ala or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Cys, Gly or Phe

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 26
Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu
1 5 10

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (3)
<223> Leu or Phe

<220>
<221> MOD_RES
<222> (4)
<223> Ser, Thr or Asn

<220>
<221> MOD_RES
<222> (5)
<223> Leu, Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Phe or Leu

<220>

279152RX

<221> MOD_RES

<222> (8)

<223> Ala or Thr

<220>

<221> MOD_RES

<222> (10)

<223> Cys, Ser or Asn

<220>

<221> MOD_RES

<222> (12)

<223> Ser, Asn or Gly

<220>

<221> MOD_RES

<222> (13)

<223> Ile or Val

<220>

<223> Description of Artificial Sequence: Consensus sequence

<400> 27

Asn His Xaa Xaa Xaa Trp Xaa Xaa Thr Xaa Leu Xaa Xaa
1 5 10

<210> 28

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> (3)

<223> Phe or Cys

<220>

<221> MOD_RES

<222> (8)

<223> Asn or Ser

<220>

<221> MOD_RES

<222> (11)

<223> His or Asn

<220>

<221> MOD_RES

<222> (12)

<223> Pro or Ser

<220>

<221> MOD_RES

<222> (13)

<223> Leu, Ile or Val

<220>

<221> MOD_RES

<222> (16)

<223> Trp or Tyr

279152RX

<220>
<223> Description of Artificial Sequence: Consensus
sequence

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1 5 10 15
Leu Lys

<210> 29
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<221> MOD_RES
<222> (4)
<223> Ile, Phe or Val

<220>
<221> MOD_RES
<222> (8)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (10)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (11)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (12)
<223> Gln or Lys

<220>
<221> MOD_RES
<222> (13)
<223> Met or Ile

<220>
<221> MOD_RES
<222> (14)
<223> Gln or Lys

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 29
Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 30
<211> 14

279152RX

<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (3)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (8)
<223> Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (10)
<223> Pro, Ser or Asn

<220>
<221> MOD_RES
<222> (13)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (14)
<223> Gln or Arg

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 30
His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa
1 5 10

<210> 31
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide translocation domain

<400> 31
Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys
1 5 10 15
Thr Gly Val Val
20